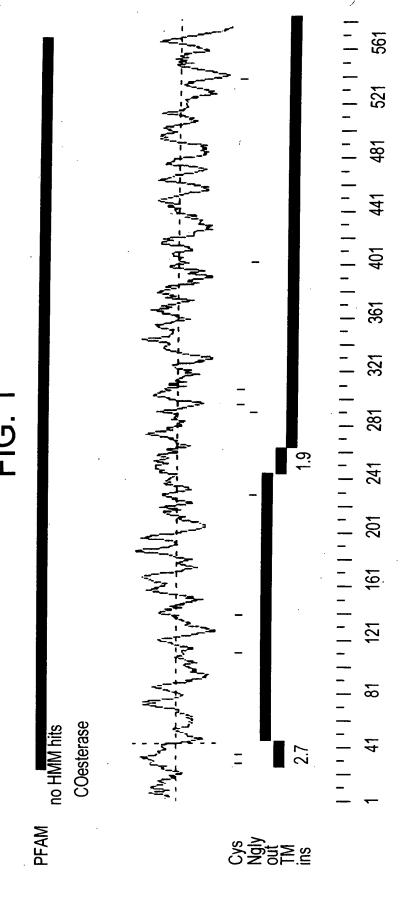


Applicant: Rosana Kapeller-Libermann, et al.
Title: METHODS OF USING 18903 TO TREAT PAIN AND PAIN-RELATED DISORDERS
Application No.: 10/001,227

Attorney/Agent: Mario Cloutier Docket No.: MP100-408P1RM

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FIG. 2A

Protein Family / Domain Matches, HMMer version

search a single seq against HMM database Searching for complete domains in PFAM HMMER 2.1.1 (Dec 1998) hmmpfam -

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HMMER is freely distributed under the GNU General Public License

/prod/ddm/seganal/PFAM/pfam6.4/Pfam HMM file:

Sequence file

Fbh18903FL Query: sequence family classification (score includes all domains) E-value Score Description Scores for Model

4.1e-164 558.6 Carboxylesterase COesterase

domains: Parsed for

E-value 4.1e-164 558.6 score 612 hmm-f hmm-t 569 seq-f seq-t 25 Domain COesterase Model

Alignments of top-scoring domains:

COesterase: domain 1 of 1, from 25 to 569: score 558.6, $\mathbf{E} = 4.1e-164$ *->mvllllfLllllliavlaaakaspedpllVatnnVlcGkvrGvnek

65 RWILCWSLTLCLMAQTALGALHT---KRPQVVTKY---GTLQGKQMH C++ C++ ++ V t++ +1+ +L 1 1 ++ +1+a+++ 25 18903

112 VGKT--PIQVFLGVPFSRPPLGILRFAPPEP-PEPWKGIRDATTYPPGCL tdngeqsvysFlGIPYAePPVGnLRFkaPqPYkepWsdvldAtkyppsCl PP+G LRF +P+P +epW++++dAt+ypp Cl ++ +F1G+P+ 99 18903



.. 1k1sEDCLYLNVytPknt

OdddfgfslsdLKvalkmlslgwnklvg..

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150	195	243	285	334	379
Q + +g+ Q-ESWGQLASMYVSTRErykwlrfsedclylnvyapara 150	kpnsklPVmVwIhGGGFmfGsghslplslYdgeslaregnVIvVsiNYRL + + +1PVmVw +GG+F +G++ s+Y g+ la++++V++V ++ RL PGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRL	GplGFLstgddklpgsGNyGLlDQrlALkWVqdNIaaFGGDPnsVTifGe G++GFLst+d+++ GN+GLlDQ +AL+WVq+NIaaFGGDP++VT+fG+ GIFGFLSTDDSHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTLFGQ 243	SAGaaSVsllllsngGDNppsskglFhRAIsqSGsalspwaiqsesnarg SAGa+S+s l++s p++ glFhRAIsqSG+al +i+s+ + SAGAMSISGLMMSPLA-SGLFHRAISQSGTALFRLFITSNPLK 285	rakelarilGCnetssselldCLRsksaeeLleatrsfilfeyvpflplf ak++a 1+GCn++s 1+ CLR s + + + + + f + + f + VAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNK-MRFLQLNFQRDP	<pre>1aFgPvvDGdDapeafipedPeelikeGkfadvPyliGvtkdEGgy ++ + +PvvDG+ +ip+dP+ 1+ +Gk + vPyl Gv++ E+ + EeiiwSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNW 379</pre>
113	151	196	244	286	335
18903	18903	18903	18903	18903	18903

LVVEEYLDNVNEHDWKMLRNRMMDIVQDATFVYA-TLQTAHYHRDAGLPV $\verb"kvlek"$ $\verb"pgdvddfsvesrkpnlqdmltDllFkcptrvaadlhakhggsPv"$ ++ ++++g Pv v e+Y++ v

faamllnasskgedelkketnpdvwlellkyllfyasealnikdMddlad

LLPYIMKFPLNR-QAMRKETITK-MLWSTRTLLN-ITKEQ-

+++ ++++

380

18903



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507 YaYvfdhpasfgigQflakrvdpefggavHgdEiffvFgnpllkeqlyka teeeeksssktmmnywanFAktGnPnngtsnglvvWpkytseeqkYslli -GIIVKPRTDGADHGDEMYFLFGGPFATG-LS v+p+++ga+HgdE++f+Fg p+ ++ 1 YLYEFEHHAR-Y+Y+f h+a+ 468 18903

MGKEKALS-LQMMKYWANFARTGNP-NDG--NLPCWPRYNKDEK--YLQL +mm+ywanFA+tGnP n++ e+++8 508

18903

llttitaqklkardprkvlonfw<-* +k1k+++ +tt

569 DFTTRVGMKLKEKK-552

18903

Searching for complete domains in SMART



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FIG. 3A

GAP of: FrGcgManager 76 IOA81nWg check: 5132 from: 1 to: 1983 Fbh18903FL - Import - vector trimmed to: FrGcgManager 76 JOA3WXZ1 check: 1319 from: 1 to: 2456 z34105 in Patent Nucleotide Symbol comparison table: /ddm local/gcg/gcg 9.1/ 1/gcgcore/data/rundata/nwsgapdna.cmp CompCheck: 8760 Gap Weight: 12 Average Match: 10.000 Length Weight: Average Mismatch: 0.000 Quality: 13796 Length: 2746 Ratio: 6.957 Gaps: 14 Percent Similarity: 92.617 Percent Identity: 92.617 Match display thresholds for the alignment(s): = IDENTITY FrGcgManager_76_IOA81nWg_ x FrGcgManager 76 JOA3WXZ1 COE-2 Z34105 101 CATTTCGCCTTGCTGACGCGTCGAGCCCTGGCCAGACATGTCCACAGGG 150 4 TTAGCCAATTCGGCCGAGGCCTCCCGCCCCAGTA.CTTGCTGGCAGGGAT 52 151 TTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACCGTGGCCGCCGGCGG 200 53 TAAGAGCAGA.TAAAAGTGTGCTCACACACTGTAGACACGGCTACCATGC 101 201 GACCAGCACAGGCGGCGTTTTCTCCTTCGGAACGGGAACGTCTAGCAACC 250 102 CATC.....CACAGTGTTGCCATCCACAGTGTTGCCATCACTCCTGC. 143 251 CTTCTGTGGGGCTCAATTTTGGAAATCTTGGAAGTACTTCAACTCCAGCA 300 144 .CCACAGCAGGAGCT..GGCTGGAGCATGAGGTGGATTCTGTG..CTGGA 188

301 ACTACATCTGCTCCTTCAAGTGGTTTTTGGAACCGGGCTCTTTTGGATCTAA 350



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FIG. 3B

189	GCCTCACCCTCTGCCTGATGGCGCAGACGGCCTTGGGTGCCTTGCAC	235
351	ACCTGCCACTGGGTTCACTCTAGGAGGA.ACAAATACAGGTGCCTTGCAC	399
236	ACCAAGAGGCCTCAAGTGGTCACCAAATATGGAACCCTGCAAGGAAAACA	285
400	ACCAAGAGGCCTCAAGTGGTCACCAAATATGGAACCCTGCAAGGAAAACA	449
286	GATGCATGTGGGGAAGACACCCATCCAAGTCTTTTTAGGAGTCCCCTTCT	335
450	GATGCATGTGGGGAAGACACCCATCCAAGTCTTTTTAGGAGTCCCCTTCT	499
336	CCAGACCTCCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCCGGAG	385
500	CCAGACCTCCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCCGGAG	549
386	CCCTGGAAAGGAATCAGAGATGCTACCACCTACCCGCCTG	425
550	CCCTGGAAAGGAATCAGAGATGCTACCACCTACCCGCCTGGATGGA	599
	· ·	
426		465
700	TGGGGCTACAGGTGCCTGCAGGAGTCCTGGGGCCAGCTGGCCTCGATGTA	749
466	CGTCAGCACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTC	515
750	CGTCAGCACGCGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTC	799
516	TGTACCTGAACGTGTACGCGCCGGGCGCGCGCGCGCGCGC	565
800	TGTACCTGAACGTGTACGCGCCGGGCGCGCGCGCGCGGGATCCCCAGCTG	849
566	CCAGTGATGGTCTGGTTCCCGGGAGGCGCCTTCATCGTGGGCGCTGCTTC	615
850		899
616	TTCGTACGAGGGCTCTGACTTGGCCGCCGCGAGAAAGTGGTGCTGGTGT	665
900	TTCGTACGAGGGCTCTGACTTGGCCGCCGCGAGAAAGTGGTGCTGT	949
666	TTCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGCACGGACGACAGC	715
950	TTCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGCACGGACGACAGC	999
716	CACGCGCGCGGGAACTGGGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTG	765



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FIG. 3C

766	GGTGCAGGAGACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCC	815
1050	GGTGCAGGAGACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCC	1099
816	TGTTCGGCCAGTCGGCGGGGCCATGAGCATCTCAGGACTGATGATGTCA	865
1100	TGTTCGGCCAGTCGGCGGGGCCATGAGCATCTCAGGACTGATGATGTCA	1149
866	CCCCTAGCCTCGGGTCTCTTCCATCGGGCCATTTCCCAGAGTGGCACCGC	915
1150		1199
916	GTTATTCAGACTTTTCATCACTAGTAACCCACTGAAAGTGGCCAAGAAGG	965
1200	GTTATTCAGACTTTTCATCACTAGTAACCCACTGAAAGTGGCCAAGAAGG	1249
966	TTGCCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAAC	1015
1250	TTGCCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAAC	1299
1016	TGCCTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGAT	1065
1300	TGCCTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTCCAACAAGAT	1349
1066	GAGATTCCTCCAACTGAACTTCCAGAGAGACCCGGAAGAGATTATCTGGT	1115
1350	GAGATTCCTCCAACTGAACTTCCAGAGAGACCCGGAAGAGATTATCTGGT	1399
1116	CCATGAGCCCTGTGGTGGTGGTGGTGATCCCAGATGACCCTTTGGTG	1165
1400	CCATGAGCCCTGTGGTGGTGGTGTGTGTGTGTG	1449
1166	CTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTTCTAGGTGTCAA	1215
1450	CTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTTCTAGGTGTCAA	1499
1216	CAACCTGGAATTCAATTGGCTCTTGCCTTATATCATGAAGTTCCCGCTAA	1265
1500		1530
	•	
1016		
	CGCACCTGTTGAATATCACCAAGGAGCAGGTACCACTTGTGGTGGAGGA	
1531	AATATCACCAAGGAGCAGGTACCACTTGTGGTCGAGGA	
1366	GTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAAACCGTA	1415



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FIG. 3D

1416	TGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCACACTGCAGACT	1465
1619	TGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCACACTGCAGACT	1668
	GCTCACTACCACCGAGATGCCGGCCTCCCTGTCTACCTGTATGAATTTGA	1515
1669	GCTCACTACCACCGA	1683
	•	
	CAACTTTGCCCGCACAGGAAACCCCAATGATGGGAATCTGCCCTGCTGGC	
1684		1716
1716	CACGCTACAACAAGGATGAAAAGTACCTGCAGCTGGATTTTACCACAAGA	1765
1717	CACGCTACAACAAGGATGAAAAGTACCTGCAGCTGGATTTTACCACAAGA	1766
1766	GTGGGCATGAAGCTCAAGGAGAAGAAGATGGCTTTTTGGATGAGTCTGTA	1815
1767	GTGGGCATGAAGCTCAAGGAGAAGAAGATGGCTTTTTGGATGAGTCTGTA	1816
1816	CCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGCTATGCA	1865
1817	CCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGCTATGCA	1866
1866	GGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGAC	1915
1867	GGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGAC	1916
1916	TAGCCATGGACATACCTGGGGACAAGAGTTCTACCCAAGGGCGAATTCGT	1965
	TAGCCATGGACATACCTGGGGACAAGAGTTCTACCCACCCCAGT	1960
1966	TTAAACCTGCAGGA.CTAG	1983
1961	TTAGAACTGCAGGAGCTCCCTGCTGCCTCCAGGCCAAAGCTAGAGCTTTT	2010

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(1989)ALIGN calculates a global alignment of two sequences version 2.0uPlease cite: Myers and Miller, CABIOS COE-2 PR0873

Global alignment score: 2271 scoring matrix: BLOSUM50, gap penalties: -12/-262.4% identity; Global alignment score: 227

COE-2	M	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		-PST1	10 PSTVLPSTVLPSLLPTAG	D.
pro873	: :: : : : : : : : : : : : : : : : : :	Vaaggtstgg 20	VFSFGTGTSS 30	::. NPSVGLNFGN 40	: :: : :	. 89 60
COE-2 pro873	20 30 40 50 60 70 AGWSMRWILCWSLTLCLMAQTALGALHTKRPQVVTKYGTLQGKQMHVGKTPIQVFLGVPF .::::::::::::::::::::::::::::::::::	40 LMAQTALGAL : : : : : : : : : : : : : : : : : :	50 HTKRPQVVTK ::::::::: HTKRPQVVTK 90	60 YGTLQGKQM: ::::::::: YGTLQGKQM: 100	40 70 MAQTALGALHTKRPQVVTKYGTLQGKQMHVGKTPIQVFLGVPF . : : : : : : : : : : : : : : : : : :	WPF ::: WPF 120
COE-2 pro873	80 90 100 110 SRPPLGILRFAPPEPPEFWKGIRDATTYPPG	100 EPWKGIRDAT :::::::: EPWKGIRDAT 140	110 TYPPG ::::: TYPPGWSLAL	SPGWSAVARS	RLTATSASRVQA(ASL 180
COE-2 pro873	LPQPLSVWG	120 WGQLASMYVS: :::::::: WGQLASMYVS: 200	130 TRERYKWLRF: ::::::::: TRERYKWLRF: 210	140 SEDCLYLNVY ::::::::::::::: SEDCLYLNVY 220	120 130 140 150	PVM ::: PVM 240

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	•			
SLLDQMA	LFRLFI :::::: LFRLFI 360	PEELIW :::::: PEELIW 420	390 MRKETI	11QTAHY :::::: 11QTAHY 510
210 DSHARGNWG :::::::: DSHARGNWG 290	270 RAISQSGTA :::::::: RAISQSGTA 350	330 FLQLNFQRI :::::::: FLQLNFQRI 410	380 MKFPLNRQ?	450 VQDATEVYAT ::::::::: VQDATEVYAT 500
200 GIFGFLSTD ::::::: GIFGFLSTD 280	260 SPLASGLFH :::::::: SPLASGLFH 340	320 VMRVSNKMR :::::::: VMRVSNKMR 400	370 EFNWLLPYT: ::::::: EFNWLLPY- 460	440 LRNRMMDIV :::::::: LRNRMMDIV 0 5
10 170 180 180 200 210 WFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMA ::::::::::::::::::::::::::::::::::::	10 230 240 250 260 270 ALRWVQENIAAFGGDFGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFI ::::::::::::::::::::::::::::::::::::	10 320 330 310 320 330 TSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNKMRFLQLNFQRDPEEIIW ::::::::::::::::::::::::::::::::::	340 350 360 370 380 39 SMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNWLLPYIMKFPLNRQAMRKETI ::::::::::::::::::::::::::::::::::::	10 410 420 430 440 450 TKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMDIVQDATFVYATLQTAHY ::::::::::::::::::::::::::::::::::::
180 GSDLAAREKV :::::::: GSDLAAREKV 260	240 NVTLFGQSAG ::::::::: NVTLFGQSAG 320	300 NHNSTQILVN ::::::::: NHNSTQILVN 380	350 LLTQGKVSSV ::::::::: LLTQGKVSSV 440	420 PLVVEEYLD ::::::: PLVVEEYLD 480
170 IVGAASSYEG :::::::: IVGAASSYEG 50	230 IAAFGGDPGN ::::::::: IAAFGGDPGN	290 KKVAHLAGCN ::::::::: KKVAHLAGCN	340 WVIPDDPLVL :::::::::: WVIPDDPLVL 30	410 TLLNITKEQV :::::: NITKEQV 470
0 VWFPGGAFIV :::::::: VWFPGGAFIV 250	ALRWVQENIA :::::::: ALRWVQENIA 310	29 TSNPLKVAKK S::::::::: SNPLKVAKK 370	34. SMSPVVDGVV SKSPVVDGVV 430	TKMLWSTRT
160 COE-2 V : pro873 V	220 COE-2 A: pro873 A:	280 COE-2 Ti pro873 Ti	COE-2 9	400 COE-2 T pro873 -



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:. pro873 -QEWA

FIG. 4C

SQRPE : :P-
570 EKKMAFWMSLYÇ : : :
560 570 DFTTRVGMKLKEKKMAFWMSLYQSQRPE ::: : : : : : : : : : : : : : : : : :
550 KDEKYLQLDFTTR :::TTR
PRYN
520 530 54(COE-2 KYWANFARTGNPNDGNLPCWI pro873
520 KYWANE



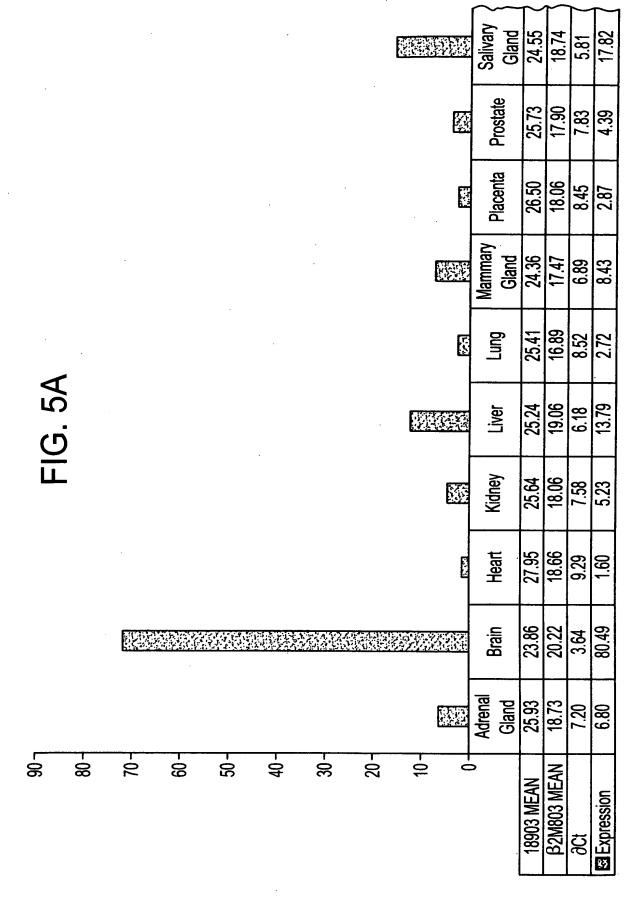
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	DRG	25.06	19.07	5.99	15.73
	Skin	23.01	17.10	5.91	16.63
	Spinal Cord	23.99	19.20	4.80	36.02
	Uterus	26.18	18.53	99.7	4.96
	Trachea	25.14	19.10	6.04	15.25
	Thymus	26.33	18.19	8.15	3.53
	Teste	24.29	19.32	4.97	31.91
受	Stomach	26.27	18.03	8.25	3.30
	Spleen	56.89	16.37	10.52	0.68
	Sm. Intestine	25.43	17.86	7.58	5.24
	\ Muscle	29.70	70.66	9.04	1.91

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REPLACEMENT SHEET

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350-

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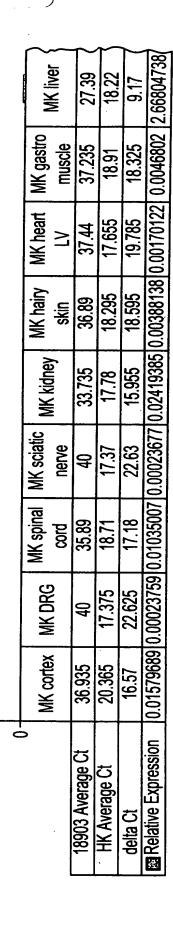
250-

700-

150-

100+

50





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Hu. Liver Hu. Lung	25.43 25.805	18.22 15.87	7.21 9.935	1.13349992 5.11872423 10.3803579 1.57002147
Hu. Kidney Hu		17.925	8.23	5.11872423 10.3
Hu. Heart	28.26	17.855	10.405	1.13349992
Hu. Spinal cord	23.78	18.295	5.485	34.3154004
Hu. Brain	(21.27	19.245	2.025	(377.618146 34.3154004

MAR 1 7 2005 BARRAGE TRADEMARKO

REPLACEMENT SHEET

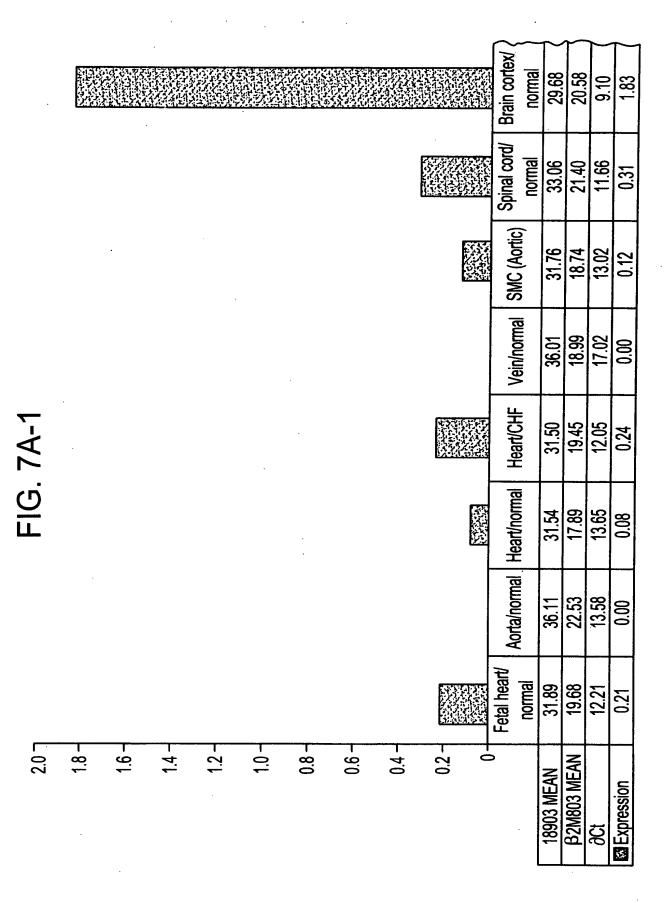
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_					
Prostate/	Tumor	29.03	17.57	11.46	0.35
Prostate/	Normal	31.16	18.34	12.83	0.14
	rancreas	30.88	17.33	13.55	0.08
OVARY/	Tumor	33.59	18.91	14.68	0.04
OVARY/	Normal	31.73	19.95	11.79	0.28
Breast tumor/	DC	30.75	17.66	13.09	0.11
Breast/	normal	30.10	18.60	11.50	0.35
Brain/	Glioblastoma	30.39	17.43	12.97	0.13
Glial cells	(Astrocytes)	33.94	21.09	12.86	0.13
Brain	hypothalamus	29.45	19.24	10.21	0.85
	Glial cells Brain/ Breast/ Breast tumor/ OVARY/ OVARY/ Prostate/	Glial cells Brain/ Breast tumor/ OVARY/ OVARY/ Pancreas Prostate/ Pancreas Normal	Glial cells Brain/ Breast/ Breast tumor/ OVARY/ OVARY/ Pancreas Prostate/ Postate/ Normal Tumor Normal Normal 33.94 30.39 30.10 30.75 31.73 33.59 30.88 31.16	Glial cells Brain/ Breast/ Breast tumor/ OVARY/ OVARY/ Pancreas Prostate/ Prostate/ Astrocytes) Glioblastoma normal IDC Normal Tumor Normal 33.94 30.39 30.10 30.75 31.73 33.59 30.88 31.16 21.09 17.43 18.60 17.66 19.95 18.91 17.33 18.34	Glial cells Brain/ Breast/ Breast tumor/ OVARY/ OVARY/ Pancreas Prostate/ Prostate/ Prostate/ (Astrocytes) Glioblastoma normal IDC Normal Tumor Normal Normal 33.94 30.39 30.10 30.75 31.73 33.59 30.88 31.16 21.09 17.43 18.60 17.66 19.95 18.91 17.33 18.34 12.86 12.97 11.50 13.09 11.79 14.68 13.55 12.83



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<u> </u>	_			_
Lung/tumor 9	30.30	17.71	12.53	0.17
Lung/normal	30.54	17.31	13.23	0.10
Fetal Liver/ normal	33.55	21.39	12.16	0.22
Liver fibrosis	30.10	18.82	11.29	0.40
Liver/normal	31.82	19.08	12.75	0.15
Kidney/ normal	30.98	20.03	10.95	0.51
Colon/iBD	32.37	17.72	14.65	0.04
Colon/normal Colon/tumor	30.80	18.15	12.66	0.16
Colon/normal	32.03	17.78	14.26	0.05



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	_ /)		_		
E-POTE ACCOUNT	Adipose/	Normal	32.43 (17.96	14.47	0.04
	Skin/Normal		31.16	20.29	10.87	0.54
	Fibroblasts	(Dermal)	33.10	18.18	14.92	0.03
	Skeletal	Muscle	31.06	18.26	12.81	0.14
(cc/stilenant)	Endothelial	Cells (Aortic)	35.27	20.16	15.11	0.03
	Epithelial Cells	(Prostate)	30.70	20.13	10.57	99:0
	Thymus/	normal	32.80	20.03	12.78	0.14
	Ly	normal	- 31.40	17.91	13.49	0.09
	nal		31.13	17.19	13.94	90:0
	Luna/COPD		(29.44	17.10	12.34	0.19



Applicant: Rosana Kapeller-Libermann, et al.

Title: METHODS OF USING 18903 TO TREAT PAIN AND PAIN-RELATED DISORDERS

Application No.: 10/001,227

Attorney/Agent: Mario Cloutier

Docket No.: MPI00-408P1RM

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						,
		HMVEC	32.74	18.74	14.00	90.0
		HUVEC	32.17	19.27	12.91	0.13
	Aorta SMC	(Late)	32.72	18.77	13.96	90.0
	Aorta SIMC	(Early)	32.50	19.53	12.97	0.13
Exert A.	7-1-1-0	Osteociasts	32.47	17.25	15.22	0.03
(E-Pietres)	Osteoblasts	(Diff)	33.23	17.83	15.40	0.02
Section 1	Osteoblasts	(Undiff)	33.19	18.50	14.69	0.04
SERVER S	Osteoblasts \	(Primary)	34.84	20.44	14.40	0.05



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Title: METHODS OF USING 18903 TO TREAT PAIN AND PAIN-RELATED

DISORDERS

Application No.: 10/001,227 Attorney/Agent: Mario Cloutier Docket No.: MPI00-408PIRM

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FIG. 7B

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Tissue 18	903 MEAN	β2M803 MEAN	δ Ct	Expression
Fetal heart/normal	31.89	19.68	12.21	0.21
Aorta/normal	36.11	22.53	13.58	0.00
Heart normal	31.54	17.89	13.65	0.08
Heart/CHF	31.50	19.45	12.05	0.24
Vein/normal	36.01	18.99	17.02	0.00
SMC (Aortic)	31.76	18.74	13.02	0.12
Spinal cord/normal	33.06	21.40	11.66	0.31
Brain cortex/normal	29.68	20.58	9.10	1.83
Brain hypothalamus/norm		19.24	10.21	0.85
Glial cells (Astrocytes		21.09	12.86	0.13
Brain/Glioblastoma	30.39	17.43	12.97	0.13
Breast/normal	30.10	18.60	11.50	0.35
Breast tumor/IDC	30.75	17.66	13.09	0.11
Ovary/normal	31.73	19.95	11.79	0.28
Ovary/tumor	33.59	18.91	14.68	0.04
Pancreas	30.88	17.33	13.55	0.04
Prostate/normal	31.16	18.34	12.83	0.14
Prostate/tumor	29.03	17.57	11.46	0.35
Colon/normal	32.03	17.78	14.26	0.05
Colon/tumor	30.80	18.15	12.66	0.16
Colon/IBD	32.37	17.72	14.65	0.04
Kidney/normal	30.98	20.03	10.95	0.51
Liver/normal	31.82	19.08	12.75	0.15
Liver/fibrosis	30.10	18.82	11.29	0.40
Fetal Liver/normal	33.55	21.39	12.16	0.40
Lung/normal	30.54	17.31	13.23	0.10
Lung/tumor	30.34	17.77	12.53	0.17
Lung/COPD	29.44	17.10	12.33	0.19
Tonsil/normal	31.13	17.19	13.94	0.06
Lymph node/normal	31.40	17.91	13.49	0.09
Thymus/normal	32.80	20.03	12.78	
Epithelial Cells(prostat		20.13	10.57	0.14
Endothelial Cells (aortic		20.16	15.11	0.66
Skeletal Muscle/normal	31.06	18.26	12.81	0.03 0.14
Fibroblasts (Dermal)	33.10	18.18		
Skin/normal			14.92	0.03
Adipose/normal	31.16	20.29	10.87	0.54
-	32.43	17.96 20.44	14.47 14.40	0.04
	34.84			0.05
Osteoblasts (Undiff)	33.19	18.50	14.69	0.04
Osteoblasts (Diff)	33.23	17.83	15.40	0.02
Osteoblasts	32.47	17.25	15.22	0.03
Aorta SMC (Early)	32.50	19.53	12.97	0.13
Aorta SMC (Late)	32.72	18.77	13.96	0.06
HUVEC	32.17	19.27	12.91	0.13
HMVEC	32.74	18.74	14.00	0.06
	40.00	40.00	,	
	40.00	40.00	0.	UU